Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application.

Listing of Claims:

1 Claim 1 (previously presented): A method for identifying a 2 transcribed region of interest of a genome comprising:

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a) Hybridizing a plurality of nucleic acid probes with a nucleic acid sample, wherein said nucleic acid sample comprises transcripts from said genome, wherein said probes are targeting an area of said genome; and

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b) Identifying said transcribed region as a region of said genome where hybridization of all consecutive probes targeting said region are above a threshold value.

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Claim 2 (original): The method of claim 1 wherein said probes are oligonucleotides.

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- Claim 3 (original): The method of claim 3 wherein said
- oligonucleotides are immobilized on a substrate.
- 1 Claim 4 (original): The method of claim 1 wherein said
- threshold is non-specific binding.
- 1 Claim 5 (currently amended): The method of claim 4 wherein
- said non-specific binding is measured using a probe designed
- 3 to contain containing at least one mismatched base.

1 Claim 6 (currently amended): The method of claim 1 further comprising:

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- c) Identifying a sub-region wherein hybridization of
 said probes targeting said <u>sub-region</u> sub regions is similar
 and, thereby indicating said sub-region as said transcribed
 region.
- 1 Claim 7 (original): The method of claim 6 wherein said
- genome is from a prokaryote.
- 1 Claim 8 (original): The method of claim 7 wherein said
- transcribed region is an operon.
- 1 Claim 9 (currently amended): The method of claim 7
- wherein said prokaryote is bacteria.

Claims 10-14 (canceled)